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# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Bisgard-Frantzen, Henrik  
Svendsen, Allan  
Borchert, Torben Vedel
- (ii) TITLE OF INVENTION: AMYLASE VARIANTS
- (iii) NUMBER OF SEQUENCES: 32
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Novo Nordisk of North America, Inc.
  - (B) STREET: 405 Lexington Avenue, Suite 6400
  - (C) CITY: New York
  - (D) STATE: New York
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 10174-6401
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/600,656
  - (B) FILING DATE: 13-FEB-1996
  - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Lambiris, Elias J.
  - (B) REGISTRATION NUMBER: 33,728
  - (C) REFERENCE/DOCKET NUMBER: 4318.204-US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 212 867 0123
  - (B) TELEFAX: 212 867 0298

## (2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 485 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |    |    |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| His | His | Asn | Gly | Thr | Asn | Gly | Thr | Met | Met | Gln | Tyr | Phe | Glu | Trp | Tyr | 1  | 5  | 10 | 15 |
| Leu | Pro | Asn | Asp | Gly | Asn | His | Trp | Asn | Arg | Leu | Arg | Asp | Asp | Ala | Ala | 20 | 25 | 30 |    |
| Asn | Leu | Lys | Ser | Lys | Gly | Ile | Thr | Ala | Val | Trp | Ile | Pro | Pro | Ala | Trp | 35 | 40 | 45 |    |
| Lys | Gly | Thr | Ser | Gln | Asn | Asp | Val | Gly | Tyr | Gly | Ala | Tyr | Asp | Leu | Tyr | 50 | 55 | 60 |    |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Leu | Gly | Glu | Phe | Asn | Gln | Lys | Gly | Thr | Val | Arg | Thr | Lys | Tyr | Gly | 65  | 70  | 75  | 80  |
| Thr | Arg | Asn | Gln | Leu | Gln | Ala | Ala | Val | Thr | Ser | Leu | Lys | Asn | Asn | Gly | 85  | 90  | 95  |     |
| Ile | Gln | Val | Tyr | Gly | Asp | Val | Val | Met | Asn | His | Lys | Gly | Gly | Ala | Asp | 100 | 105 | 110 |     |
| Gly | Thr | Glu | Ile | Val | Asn | Ala | Val | Glu | Val | Asn | Arg | Ser | Asn | Arg | Asn | 115 | 120 | 125 |     |
| Gln | Glu | Thr | Ser | Gly | Glu | Tyr | Ala | Ile | Glu | Ala | Trp | Thr | Lys | Phe | Asp | 130 | 135 | 140 |     |
| Phe | Pro | Gly | Arg | Gly | Asn | Asn | His | Ser | Ser | Phe | Lys | Trp | Arg | Trp | Tyr | 145 | 150 | 155 | 160 |
| His | Phe | Asp | Gly | Thr | Asp | Trp | Asp | Gln | Ser | Arg | Gln | Leu | Gln | Asn | Lys | 165 | 170 | 175 |     |
| Ile | Tyr | Lys | Phe | Arg | Gly | Thr | Gly | Lys | Ala | Trp | Asp | Trp | Glu | Val | Asp | 180 | 185 | 190 |     |
| Thr | Glu | Asn | Gly | Asn | Tyr | Asp | Tyr | Leu | Met | Tyr | Ala | Asp | Val | Asp | Met | 195 | 200 | 205 |     |
| Asp | His | Pro | Glu | Val | Ile | His | Glu | Leu | Arg | Asn | Trp | Gly | Val | Trp | Tyr | 210 | 215 | 220 |     |
| Thr | Asn | Thr | Leu | Asn | Leu | Asp | Gly | Phe | Arg | Ile | Asp | Ala | Val | Lys | His | 225 | 230 | 235 | 240 |
| Ile | Lys | Tyr | Ser | Phe | Thr | Arg | Asp | Trp | Leu | Thr | His | Val | Arg | Asn | Thr | 245 | 250 | 255 |     |
| Thr | Gly | Lys | Pro | Met | Phe | Ala | Val | Ala | Glu | Phe | Trp | Lys | Asn | Asp | Leu | 260 | 265 | 270 |     |
| Gly | Ala | Ile | Glu | Asn | Tyr | Leu | Asn | Lys | Thr | Ser | Trp | Asn | His | Ser | Val | 275 | 280 | 285 |     |
| Phe | Asp | Val | Pro | Leu | His | Tyr | Asn | Leu | Tyr | Asn | Ala | Ser | Asn | Ser | Gly | 290 | 295 | 300 |     |
| Gly | Tyr | Tyr | Asp | Met | Arg | Asn | Ile | Leu | Asn | Gly | Ser | Val | Val | Gln | Lys | 305 | 310 | 315 | 320 |
| His | Pro | Thr | His | Ala | Val | Thr | Phe | Val | Asp | Asn | His | Asp | Ser | Gln | Pro | 325 | 330 | 335 |     |
| Gly | Glu | Ala | Leu | Glu | Ser | Phe | Val | Gln | Gln | Trp | Phe | Lys | Pro | Leu | Ala | 340 | 345 | 350 |     |
| Tyr | Ala | Leu | Val | Leu | Thr | Arg | Glu | Gln | Gly | Tyr | Pro | Ser | Val | Phe | Tyr | 355 | 360 | 365 |     |
| Gly | Asp | Tyr | Tyr | Gly | Ile | Pro | Thr | His | Gly | Val | Pro | Ala | Met | Lys | Ser | 370 | 375 | 380 |     |
| Lys | Ile | Asp | Pro | Leu | Leu | Gln | Ala | Arg | Gln | Thr | Phe | Ala | Tyr | Gly | Thr | 385 | 390 | 395 | 400 |
| Gln | His | Asp | Tyr | Phe | Asp | His | His | Asp | Ile | Ile | Gly | Trp | Thr | Arg | Glu | 405 | 410 | 415 |     |

Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp  
420 425 430

Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly  
435 440 445

Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile  
450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser  
465 470 475 480

Val Trp Val Lys Gln  
485

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His  
1 5 10 15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser  
20 25 30

Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp  
35 40 45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr  
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly  
65 70 75 80

Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly  
85 90 95

Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp  
100 105 110

Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn  
115 120 125

Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp  
130 135 140

Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr  
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg  
165 170 175

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp  
180 185 190

Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met  
195 200 205

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Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr  
 210 215 220  
 Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His  
 225 230 235 240  
 Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala  
 245 250 255  
 Thr Gly Lys Glu Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu  
 260 265 270  
 Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val  
 275 280 285  
 Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly  
 290 295 300  
 Gly Asn Tyr Asp Met Ala Lys Leu Leu Asn Gly Thr Val Val Gln Lys  
 305 310 315 320  
 His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro  
 325 330 335  
 Gly Glu Ser Leu Glu Ser Phe Val Gln Glu Trp Phe Lys Pro Leu Ala  
 340 345 350  
 Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr  
 355 360 365  
 Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala  
 370 375 380  
 Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr  
 385 390 395 400  
 Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu  
 405 410 415  
 Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp  
 420 425 430  
 Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly  
 435 440 445  
 Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile  
 450 455 460  
 Asn Ala Asp Gly Trp Ala Asn Phe Ser Val Asn Gly Gly Ser Val Ser  
 465 470 475 480  
 Ile Trp Val Lys Arg  
 485

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 514 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

0902188-071001

Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr Leu  
1 5 10 15  
Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn  
20 25 30  
Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys  
35 40 45  
Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp  
50 55 60  
Leu Gly Glu Phe Asn Gln Lys Gly Ala Val Arg Thr Lys Tyr Gly Thr  
65 70 75 80  
Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met  
85 90 95  
Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly  
100 105 110  
Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln  
115 120 125  
Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe  
130 135 140  
Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His  
145 150 155 160  
Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr  
165 170 175  
Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu  
180 185 190  
Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His  
195 200 205  
Pro Glu Val Val Thr Glu Leu Lys Ser Trp Gly Lys Trp Tyr Val Asn  
210 215 220  
Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys  
225 230 235 240  
Phe Ser Phe Phe Pro Asp Trp Leu Ser Asp Val Arg Ser Gln Thr Gly  
245 250 255  
Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys  
260 265 270  
Leu His Asn Tyr Ile Met Lys Thr Asn Gly Thr Met Ser Leu Phe Asp  
275 280 285  
Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Thr  
290 295 300  
Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro  
305 310 315 320  
Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln  
325 330 335  
Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala  
340 345 350

[illegible]

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1455 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

|            |            |             |             |             |            |     |
|------------|------------|-------------|-------------|-------------|------------|-----|
| CATCATAATG | GAACAAATGG | TACTATGATG  | CAATATTTTCG | AATGGTATTT  | GCCAAATGAC | 60  |
| GGGAATCATT | GGAACAGGTT | GAGGGATGAC  | GCAGCTAACT  | TAAAGAGTAA  | AGGGATAACA | 120 |
| GCTGTATGGA | TCCCACCTGC | ATGGAAGGGG  | ACTTCCCAGA  | ATGATGTAGG  | TTATGGAGCC | 180 |
| TATGATTTAT | ATGATCTTGG | AGAGTTTAAAC | CAGAAGGGGA  | CGGTTTCGTAC | AAAATATGGA | 240 |
| ACACGCAACC | AGCTACAGGC | TGCGGTGACC  | TCTTTAAAAA  | ATAACGGCAT  | TCAGGTATAT | 300 |
| GGTGATGTCT | TCATGAATCA | TAAAGGTGGA  | GCAGATGGTA  | CGGAAATTGT  | AAATGCGGTA | 360 |
| GAAGTGAATC | GGAGCAACCG | AAACCAGGAA  | ACCTCAGGAG  | AGTATGCAAT  | AGAAGCGTGG | 420 |
| ACAAAGTTTG | ATTTTCCTGG | AAGAGGAAAT  | AACCATTCCA  | GCTTTAAGTG  | GCGCTGGTAT | 480 |
| CATTTTGATG | GGACAGATTG | GGATCAGTCA  | CGCCAGCTTC  | AAAACAAAAT  | ATATAAATTC | 540 |
| AGGGGAACAG | GCAAGGCCTG | GGACTGGGAA  | GTCGATACAG  | AGAATGGCAA  | CTATGACTAT | 600 |
| CTTATGTATG | CAGACGTGGA | TATGGATCAC  | CCAGAAGTAA  | TACATGAACT  | TAGAAACTGG | 660 |

GGAGTGTGGT ATACGAATAC ACTGAACCTT GATGGATTTA GAATAGATGC AGTGAAACAT 720  
 ATAAATATA GCTTTACGAG AGATTGGCTT ACACATGTGC GTAACACCAC AGGTAAACCA 780  
 ATGTTTGCAG TGGCTGAGTT TTGGAAAAAT GACCTTGGTG CAATTGAAAA CTATTTGAAT 840  
 AAAACAAGTT GGAATCACTC GGTGTTTGAT GTTCCTCTCC ACTATAATTT GTACAATGCA 900  
 TCTAATAGCG GTGGTTATTA TGATATGAGA AATATTTTAA ATGGTTCTGT GGTGCAAAAA 960  
 CATCCAACAC ATGCCGTTAC TTTTGTTGAT AACCATGATT CTCAGTCCGG GGAAGCATTG 1020  
 GAATCCTTTG TTCAACAATG GTTTAAACCA CTTGCATATG CATTGGTTCT GACAAGGGAA 1080  
 CAAGGTTATC CTTCCGTATT TTATGGGGAT TACTACGGTA TCCCAACCCA TGGTGTTCGG 1140  
 GCTATGAAAT CTAAAATAGA CCCTCTTCTG CAGGCACGTC AAACCTTTGC CTATGGTACG 1200  
 CAGCATGATT ACTTTGATCA TCATGATATT ATCGGTTGGA CAAGAGAGGG AAATAGCTCC 1260  
 CATCCAAATT CAGGCCTTGC CACCATTATG TCAGATGGTC CAGGTGGTAA CAAATGGATG 1320  
 TATGTGGGGA AAAATAAAGC GGGACAAGTT TGGAGAGATA TTACCGGAAA TAGGACAGGC 1380  
 ACCGTCACAA TTAATGCAGA CGGATGGGGT AATTTCTCTG TTAATGGAGG GTCCGTTTCG 1440  
 GTTTGGGTGA AGCAA 1455

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1455 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CATCATAATG GGACAAATGG GACGATGATG CAATACTTTG AATGGCACTT GCCTAATGAT 60  
 GGGAATCACT GGAATAGATT AAGAGATGAT GCTAGTAATC TAAGAAATAG AGGTATAACC 120  
 GCTATTTGGA TTCCGCCTGC CTGGAAAGGG ACTTCGCAAA ATGATGTGGG GTATGGAGCC 180  
 TATGATCTTT ATGATTTAGG GGAATTTAAT CAAAAGGGGA CGGTTTCGTAC TAAGTATGGG 240  
 ACACGTAGTC AATTGGAGTC TGCCATCCAT GCTTTAAAGA ATAATGGCGT TCAAGTTTAT 300  
 GGGGATGTAG TGATGAACCA TAAAGGAGGA GCTGATGCTA CAGAAAACGT TCTTGCTGTC 360  
 GAGGTGAATC CAAATAACCG GAATCAAGAA ATATCTGGGG ACTACACAAT TGAGGCTTGG 420  
 ACTAAGTTTG ATTTTCCAGG GAGGGGTAAT ACATACTCAG ACTTTAAATG GCGTTGGTAT 480  
 CATTTCGATG GTGTAGATTG GGATCAATCA CGACAATTCC AAAATCGTAT CTACAAATTC 540  
 CGAGGTGATG GTAAGGCATG GGATTGGGAA GTAGATTCGG AAAATGGAAA TTATGATTAT 600  
 TTAATGTATG CAGATGTAGA TATGGATCAT CCGGAGGTAG TAAATGAGCT TAGAAGATGG 660  
 GGAGAATGGT ATACAAATAC ATTAAATCTT GATGGATTTA GGATCGATGC GGTGAAGCAT 720  
 ATTAAATATA GCTTTACACG TGATTGGTTG ACCCATGTAA GA/ACGCAAC GGGAAAAGAA 780



|   |      |
|---|------|
| ATGTTTGCTG TTGCTGAATT TTGGAAAAAT GATTTAGGTG CCTTGGAGAA CTATTTAAAT | 840  |
| AAAACAAACT GGAATCATTG TGTCTTTGAT GTCCCCCTTC ATTATAATCT TTATAACGCG | 900  |
| TCAAATAGTG GAGGCAACTA TGACATGGCA AACTTCTTA ATGAAACGGT TGTTCAAAAG  | 960  |
| CATCCAATGC ATGCCGTAAC TTTTGTGGAT AATCACGATT CTCAACCTGG GGAATCATTG | 1020 |
| GAATCATTTG TACAAGAATG GTTTAAGCCA CTTGCTTATG CGCTTATTTT AACAAGAGAA | 1080 |
| CAAGGCTATC CCTCTGTCTT CTATGGTGAC TACTATGGAA TTCCAACACA TAGTGTCCCA | 1140 |
| GCAATGAAAG CCAAGATTGA TCCAATCTTA GAGGCGCGTC AAAATTTTGC ATATGGAACA | 1200 |
| CAACATGATT ATTTTGACCA TCATAATATA ATCGGATGGA CACGTGAAGG AAATACCACG | 1260 |
| CATCCCAATT CAGGACTTGC GACTATCATG TCGGATGGGC CAGGGGGAGA GAAATGGATG | 1320 |
| TACGTAGGGC AAAATAAAGC AGGTCAAGTT TGGCATGACA TAACTGGAAA TAAACCAGGA | 1380 |
| ACAGTTACGA TCAATGCAGA TGGATGGGCT AATTTTTCAG TAAATGGAGG ATCTGTTTCC | 1440 |
| ATTGGGTGA AACGA   | 1455 |

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1548 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

|   |     |
|---|-----|
| GCCGCACCGT TTAACGGCAC CATGATGCAG TATTTTGAAT GGTACTTGCC GGATGATGGC | 60  |
| ACGTTATGGA CCAAAGTGGC CAATGAAGCC AACAACTTAT CCAGCCTTGG CATCACCGCT | 120 |
| CTTTGGCTGC CGCCCGCTTA CAAAGGAACA AGCCGCAGCG ACGTAGGGTA CGGAGTATAC | 180 |
| GACTTGTATG ACCTCGGCGA ATTCAATCAA AAAGGGACCG TCCGCACAAA ATACGGAACA | 240 |
| AAAGCTCAAT ATCTTCAAGC CATTCAAGCC GCCCAGCCG CTGGAATGCA AGTGACGCC   | 300 |
| GATGTCGTGT TCGACCATAA AGGCGGCGCT GACGGCACGG AATGGGTGGA CGCCGTCGAA | 360 |
| GTCAATCCGT CCGACCGCAA CCAAGAAATC TCGGGCACCT ATCAAATCCA AGCATGGACG | 420 |
| AAATTTGATT TTCCCGGGCG GGGCAACACC TACTCCAGCT TTAAGTGGCG CTGGTACCAT | 480 |
| TTTGACGGCG TTGATTGGGA CGAAAGCCGA AAATTGAGCC GCATTTACAA ATTCCGCGGC | 540 |
| ATCGGCAAAG CGTGGGATTG GGAAGTAGAC ACGGAAAACG GAACTATGA CTACTTAATG  | 600 |
| TATGCCGACC TTGATATGGA TCATCCCGAA GTCGTGACCG AGCTGAAAAA CTGGGGGAAA | 660 |
| TGGTATGTCA ACACAACGAA CATTGATGGG TTCCGGCTTG ATGCCGTCAA GCATATTAAG | 720 |
| TTCAGTTTTT TTCCTGATTG GTTGTCTGAT GTGCGTTCTC AGACTGGCAA GCCGCTATTT | 780 |
| ACCGTCGGGG AATATTGGAG CTATGACATC AACAAATTGC ACAATTACAT TACGAAAACA | 840 |
| GACGGAACGA TGTCTTTGTT TGATGCCCCG TTACACAACA AATTTTATAC CGCTTCCAAA | 900 |

TCAGGGGGCG CATTGTATAT GCGCACGTTA ATGACCAATA CTCTCATGAA AGATCAACCG 960  
ACATTGGCCG TCACCTTCGT TGATAATCAT GACACCGAAC CCGGCCAAGC GCTGCAGTCA 1020  
TGGGTGCGACC CATGGTTCAA ACCGTTGGCT TACGCCTTTA TTCTAACTCG GCAGGAAGGA 1080  
TACCCGTGCG TCTTTTATGG TGACTATTAT GGCATTCCAC AATATAACAT TCCTTCGCTG 1140  
AAAAGCAAAA TCGATCCGCT CCTCATCGCG CGCAGGGATT ATGCTTACGG AACGCAACAT 1200  
GATTATCTTG ATCACTCCGA CATCATCGGG TGGACAAGGG AAGGGGGCAC TGAAAAACCA 1260  
GGATCCGGAC TGGCCGCACT GATCACCGAT GGGCCGGGAG GAAGCAAATG GATGTACGTT 1320  
GGCAAACAAC ACGCTGGAAG AGTGTCTAT GACCTTACCG GCAACCGGAG TGACACCGTC 1380  
ACCATCAACA GTGATGGATG GGGGGAATTC AAAGTCAATG GCGGTTCGGT TTCGGTTTGG 1440  
GTTCTAGAA AAACGACCGT TTCTACCATC GCTCGGCCGA TCACAACCCG ACCGTGGACT 1500  
GGTGAATTCTG TCCGTTGGAC CGAACCACGG TTGGTGGCAT GGCCTTGA 1548

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear.

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | His | Asn | Gly | Thr | Asn | Gly | Thr | Met | Met | Gln | Tyr | Phe | Glu | Trp | Tyr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Pro | Asn | Asp | Gly | Asn | His | Trp | Asn | Arg | Leu | Asn | Ser | Asp | Ala | Ser |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asn | Leu | Lys | Ser | Lys | Gly | Ile | Thr | Ala | Val | Trp | Ile | Pro | Pro | Ala | Trp |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Lys | Gly | Ala | Ser | Gln | Asn | Asp | Val | Gly | Tyr | Gly | Ala | Tyr | Asp | Leu | Tyr |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Asp | Leu | Gly | Glu | Phe | Asn | Gln | Lys | Gly | Thr | Val | Arg | Thr | Lys | Tyr | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Arg | Ser | Gln | Leu | Gln | Ala | Ala | Val | Thr | Ser | Leu | Lys | Asn | Asn | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Gln | Val | Tyr | Gly | Asp | Val | Val | Met | Asn | His | Lys | Gly | Gly | Ala | Asp |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ala | Thr | Glu | Met | Val | Arg | Ala | Val | Glu | Val | Asn | Pro | Asn | Asn | Arg | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Gln | Glu | Val | Thr | Gly | Glu | Tyr | Thr | Ile | Glu | Ala | Trp | Thr | Arg | Phe | Asp |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Phe | Pro | Gly | Arg | Gly | Asn | Thr | His | Ser | Ser | Phe | Lys | Trp | Arg | Trp | Tyr |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| His | Phe | Asp | Gly | Val | Asp | Trp | Asp | Gln | Ser | Arg | Arg | Leu | Asn | Asn | Arg |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Tyr | Lys | Phe | Arg | Gly | His | Gly | Lys | Ala | Trp | Asp | Trp | Glu | Val | Asp | 180 | 185 | 190 |
| Thr | Glu | Asn | Gly | Asn | Tyr | Asp | Tyr | Leu | Met | Tyr | Ala | Asp | Ile | Asp | Met | 195 | 200 | 205 |
| Asp | His | Pro | Glu | Val | Val | Asn | Glu | Leu | Arg | Asn | Trp | Gly | Val | Trp | Tyr | 210 | 215 | 220 |
| Thr | Asn | Thr | Leu | Gly | Leu | Asp | Gly | Phe | Arg | Ile | Asp | Ala | Val | Lys | His | 225 | 230 | 235 |
| Ile | Lys | Tyr | Ser | Phe | Thr | Arg | Asp | Trp | Ile | Asn | His | Val | Arg | Ser | Ala | 245 | 250 | 255 |
| Thr | Gly | Lys | Asn | Met | Phe | Ala | Val | Ala | Glu | Phe | Trp | Lys | Asn | Asp | Leu | 260 | 265 | 270 |
| Gly | Ala | Ile | Glu | Asn | Tyr | Leu | Gln | Lys | Thr | Asn | Trp | Asn | His | Ser | Val | 275 | 280 | 285 |
| Phe | Asp | Val | Pro | Leu | His | Tyr | Asn | Leu | Tyr | Asn | Ala | Ser | Lys | Ser | Gly | 290 | 295 | 300 |
| Gly | Asn | Tyr | Asp | Met | Arg | Asn | Ile | Phe | Asn | Gly | Thr | Val | Val | Gln | Arg | 305 | 310 | 315 |
| His | Pro | Ser | His | Ala | Val | Thr | Phe | Val | Asp | Asn | His | Asp | Ser | Gln | Pro | 325 | 330 | 335 |
| Glu | Glu | Ala | Leu | Glu | Ser | Phe | Val | Glu | Glu | Trp | Phe | Lys | Pro | Leu | Ala | 340 | 345 | 350 |
| Tyr | Ala | Leu | Thr | Leu | Thr | Arg | Glu | Gln | Gly | Tyr | Pro | Ser | Val | Phe | Tyr | 355 | 360 | 365 |
| Gly | Asp | Tyr | Tyr | Gly | Ile | Pro | Thr | His | Gly | Val | Pro | Ala | Met | Arg | Ser | 370 | 375 | 380 |
| Lys | Ile | Asp | Pro | Ile | Leu | Glu | Ala | Arg | Gln | Lys | Tyr | Ala | Tyr | Gly | Lys | 385 | 390 | 395 |
| Gln | Asn | Asp | Tyr | Leu | Asp | His | His | Asn | Ile | Ile | Gly | Trp | Thr | Arg | Glu | 405 | 410 | 415 |
| Gly | Asn | Thr | Ala | His | Pro | Asn | Ser | Gly | Leu | Ala | Thr | Ile | Met | Ser | Asp | 420 | 425 | 430 |
| Gly | Ala | Gly | Gly | Ser | Lys | Trp | Met | Phe | Val | Gly | Arg | Asn | Lys | Ala | Gly | 435 | 440 | 445 |
| Gln | Val | Trp | Ser | Asp | Ile | Thr | Gly | Asn | Arg | Thr | Gly | Thr | Val | Thr | Ile | 450 | 455 | 460 |
| Asn | Ala | Asp | Gly | Trp | Gly | Asn | Phe | Ser | Val | Asn | Gly | Gly | Ser | Val | Ser | 465 | 470 | 475 |
| Ile | Trp | Val | Asn | Lys |     |     |     |     |     |     |     |     |     |     |     | 485 |     |     |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTGCGGTGA CCTCTTTAAA AAATAACGGC

30

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCACCGCTAT TAGATGCATT GTAC

24

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTTACGTATG CAGACGTCGA TATGGATCAC CC

32

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATCCATATC GACGTCTGCA TACGTAAGAT AGTC

34

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTASGGGCAA GGCCTGGGAC TGG

23

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCCAGGCCTT GCCCSTAAAT TTATATATTT TGTTTTG

37

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGTTTCGGTT CGAAGGATTC ACTTCTACCG C

31

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGGTAGAAG TGAATCCTTC GAACCGAAAC CAG

33

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTACTATCG TAACAATGGC CGATTGCTGA CGCTGTTATT TGC

43

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTGTGACTGG TGAGTACTCA ACCAAGTC

28

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTACTTCCCA ATCCCAAGCT TTACCTCGGA ATTTG

35

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAAATTCCGA GGTAAAGCTT GGGATTGGGA AGTAG

35

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTGAACAACC GTTCCATTAA GAAG

24

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTCTGTATCG ACTTCCAGT CCAAGCTTT TGTCCTGAAT TTATATATT TGTTTTGAAG

60

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTCTGTATCG ACTTCCAGT CCAAGCTTT GCCTCCGAAT TTATATATT TGTTTTGAAG

60

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATGTGTAAGC CAATCGCGAG TAAAGCTAAA TTTTATATGT TTCACTGCAT C

51

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCACCAAGGT CATTCGCCA GAATTCAGCC ACTG

34

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGTCAGAACC AACGCGTATG CACATGGTTT AAACCATTG

39

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ACCACCTGGA CCATCGCTGC AGATGGTGGC AAGGCCTGAA TT

42

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGCAAAAGTT TGACGTGCCT CGAGAAGAGG GTCTAT

36

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TTGTCCCGCT TTATTCTGGC CAACATACAT CCATT

36

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCCAATCCCA AGCTTTACCA YCGAACTTGT AGATACG

37

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCCAATCCCA AGCTTTATCT CSGAACTTGT AGATACG

37

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GATCCATATC GACGTCTGCA TACAGTAAAT AATC

34

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GATCCATATC GACGTCTGCA TAAATTAAAT AATC